FIG. 1

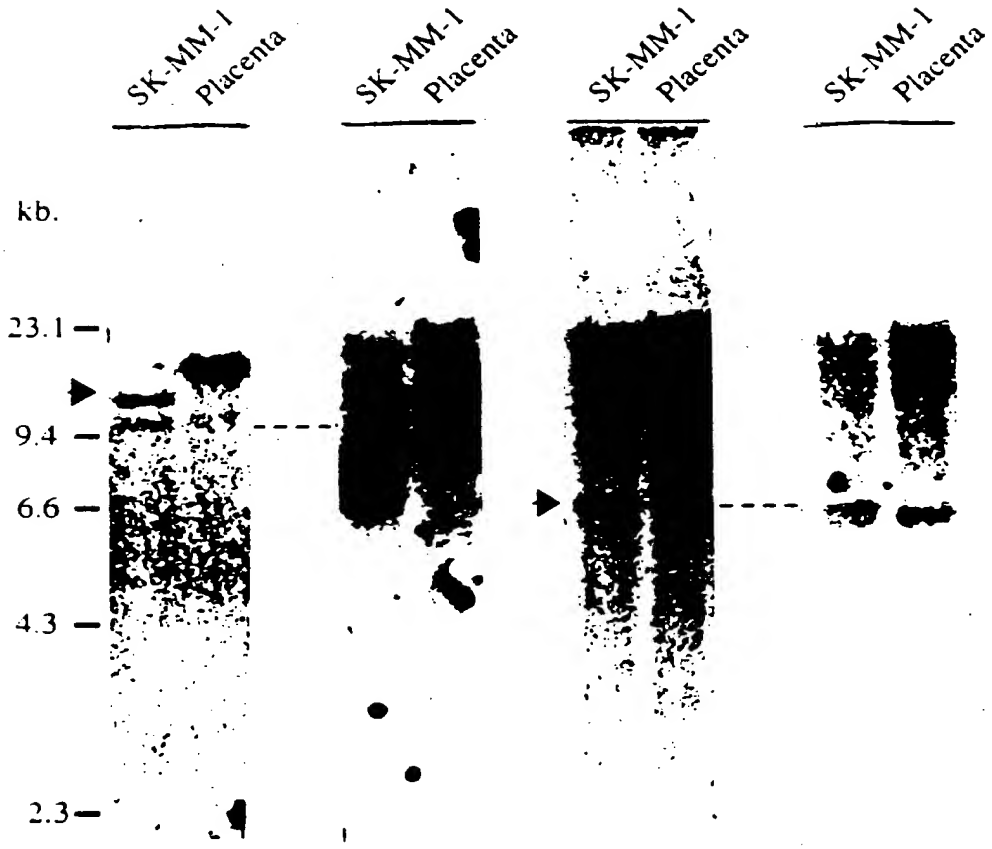

SK-MM-1
Placenta
SK-MM-1
Placenta
SK-MM-1
Placenta
SK-MM-1
Placenta
kb.
23.1
9.4
6.6
4.3
2.3
JH
Cγ2
Cμ
0.7B/H
BamHI

FIG. 2A

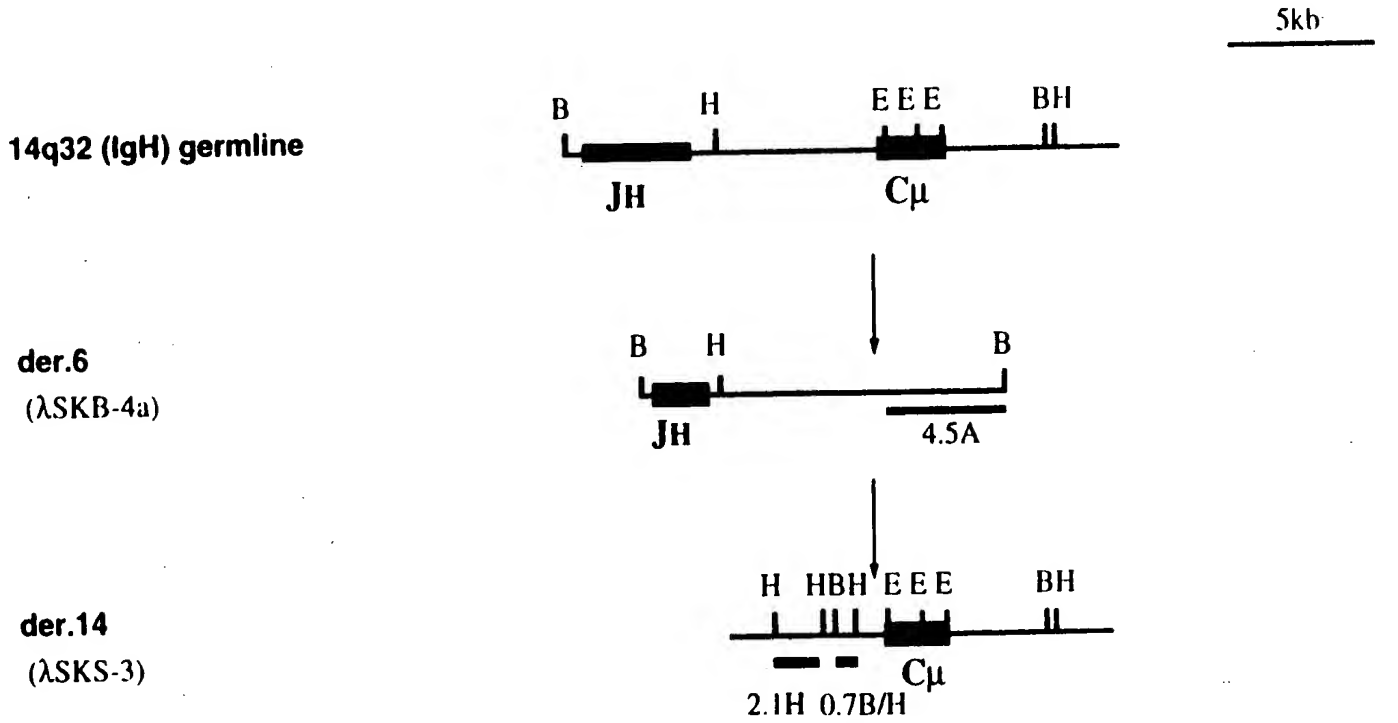

5kb
14q32 (IgH) germline
B
H
E E E
BH
JH
Cμ
der.6
(λSKB-4a)
B
H
B
JH
4.5A
der.14
(λSKS-3)
H
HBH
E E E
BH
Cμ
2.1H
0.7B/H
6p25 germline
HB E
E
E
H
E
EHB
H
HBH
B
B
E
H
λMUM-3
λMUM-4

FIG. 2B

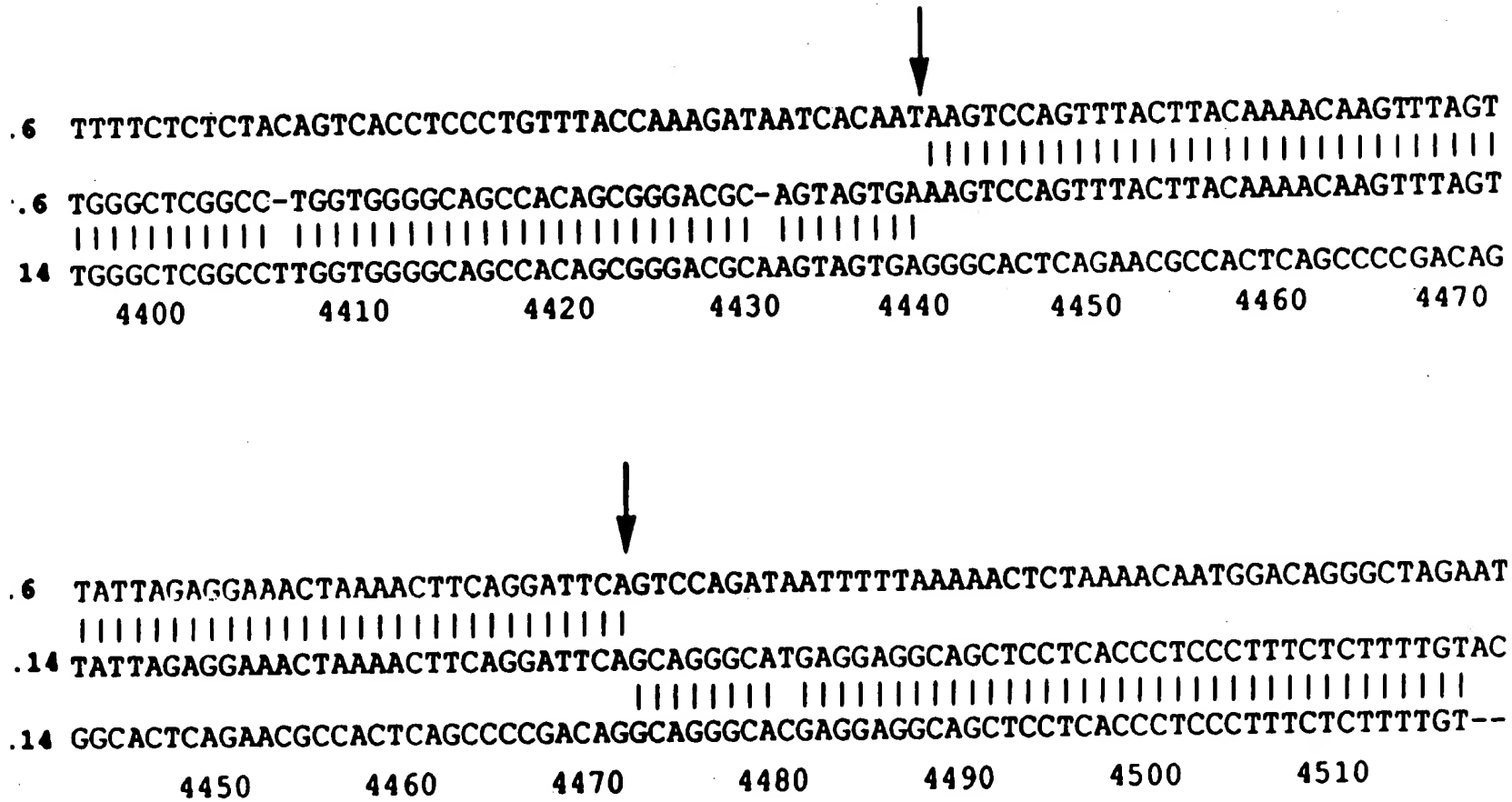

.6 TTTTCTCTCTACAGTCACCTCCCTGTTTACCAAAGATAATCACAATAAGTCCAGTTTACTTACAAAACAAGTTTAGT
.6 TGGGCTCGGCC-TGGTGGGGCAGCCACAGCGGGACGC-AGTAGTGAAAGTCCAGTTTACTTACAAAACAAGTTTAGT
14 TGGGCTCGGCCTTGGTGGGGCAGCCACAGCGGGACGCAAGTAGTGAGGGCACTCAGAACGCCACTCAGCCCCGACAG
4400 4410 4420 4430 4440 4450 4460 4470
.6 TATTAGAGGAAACTAAAACTTCAGGATTCAGTCCAGATAATTTTTAAAAACTCTAAAACAATGGACAGGGCTAGAAT
.14 TATTAGAGGAAACTAAAACTTCAGGATTCAGCAGGGCATGAGGAGGCAGCTCCTCACCCTCCCTTTCTCTTTTGTAC
.14 GGCACTCAGAACGCCACTCAGCCCCGACAGGCAGGGCACGAGGAGGCAGCTCCTCACCCTCCCTTTCTCTTTTGT--
4450 4460 4470 4480 4490 4500 4510

FIG. 3A

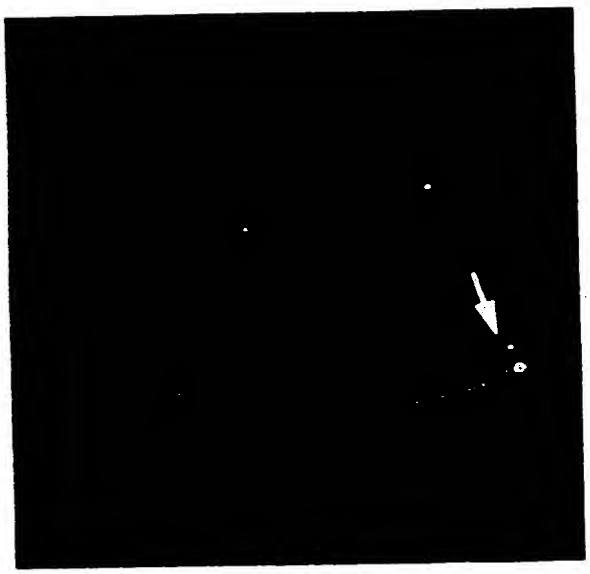


FIG. 3B

λMUM-3

FIG. 4A

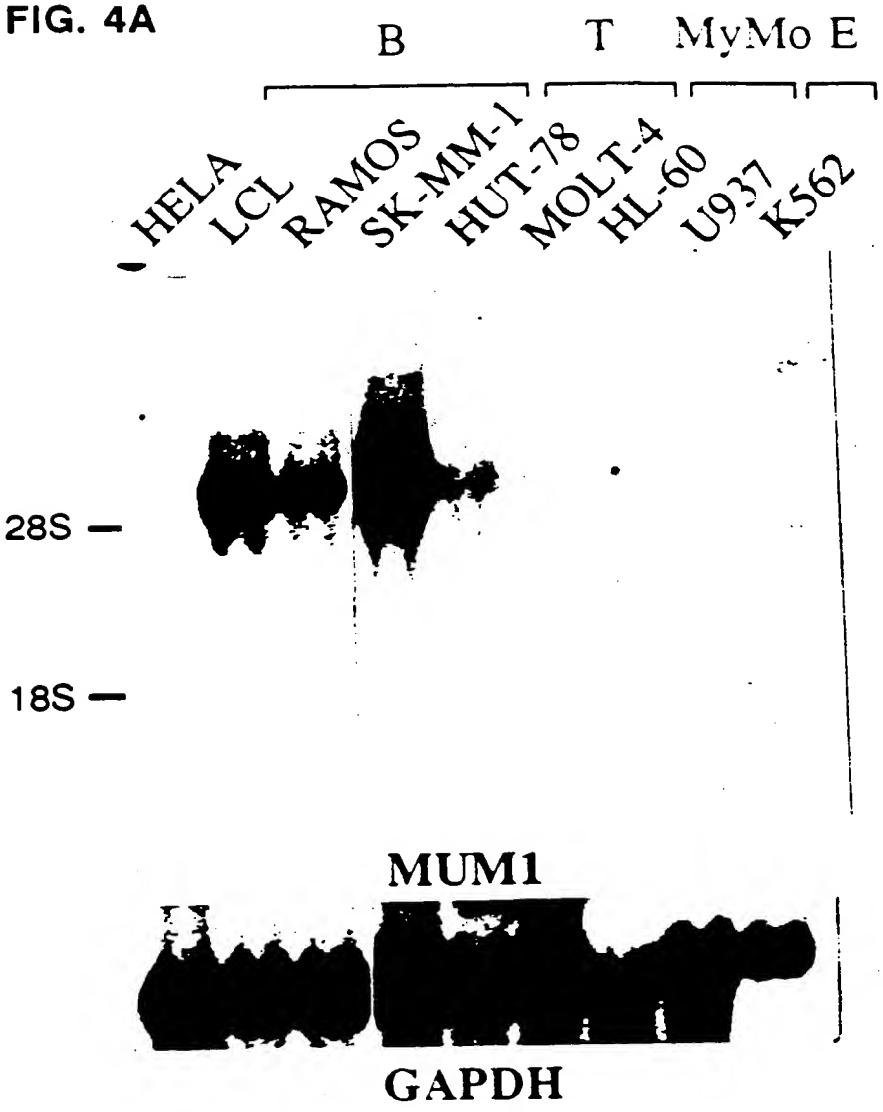

B
T
MyMo
E
HELA
LCL
RAMOS
SK-MM-1
HUT-78
MOLT-4
HL-60
U937
K562
28S
18S
MUM1
GAPDH

FIG. 4B

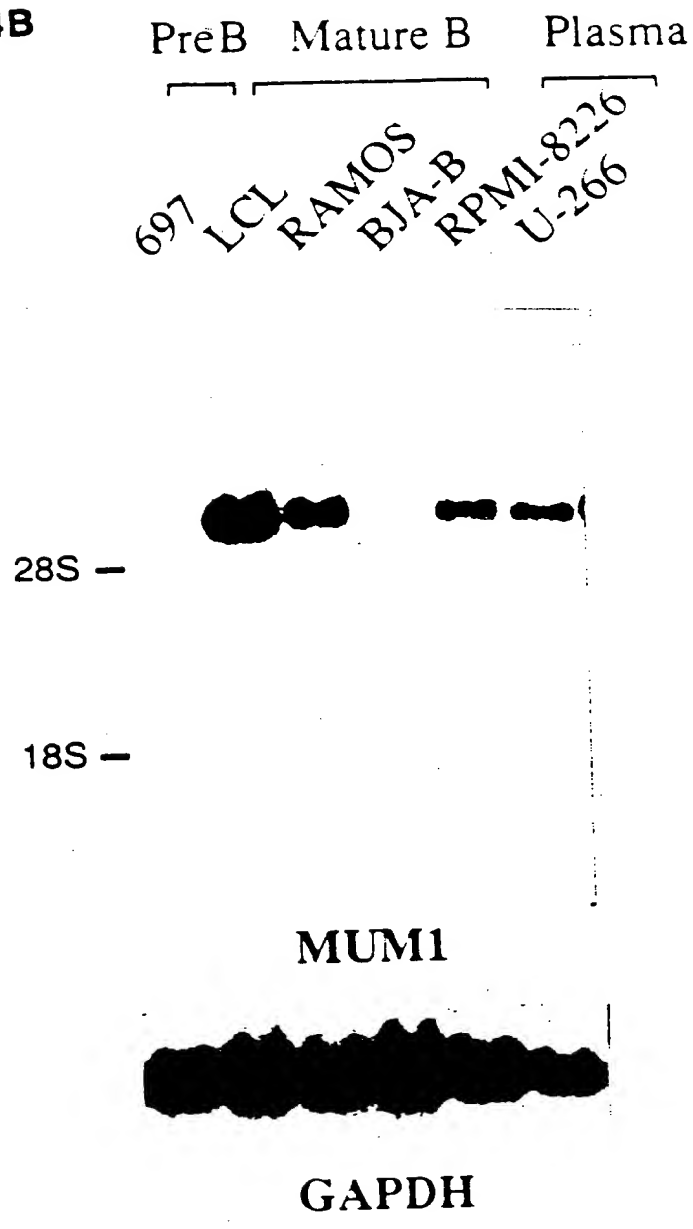

Pre B
Mature B
Plasma
697
LCL
RAMOS
BJA-B
RPMI-8226
U-266
28S
18S
MUM1
GAPDH

FIG. 4C

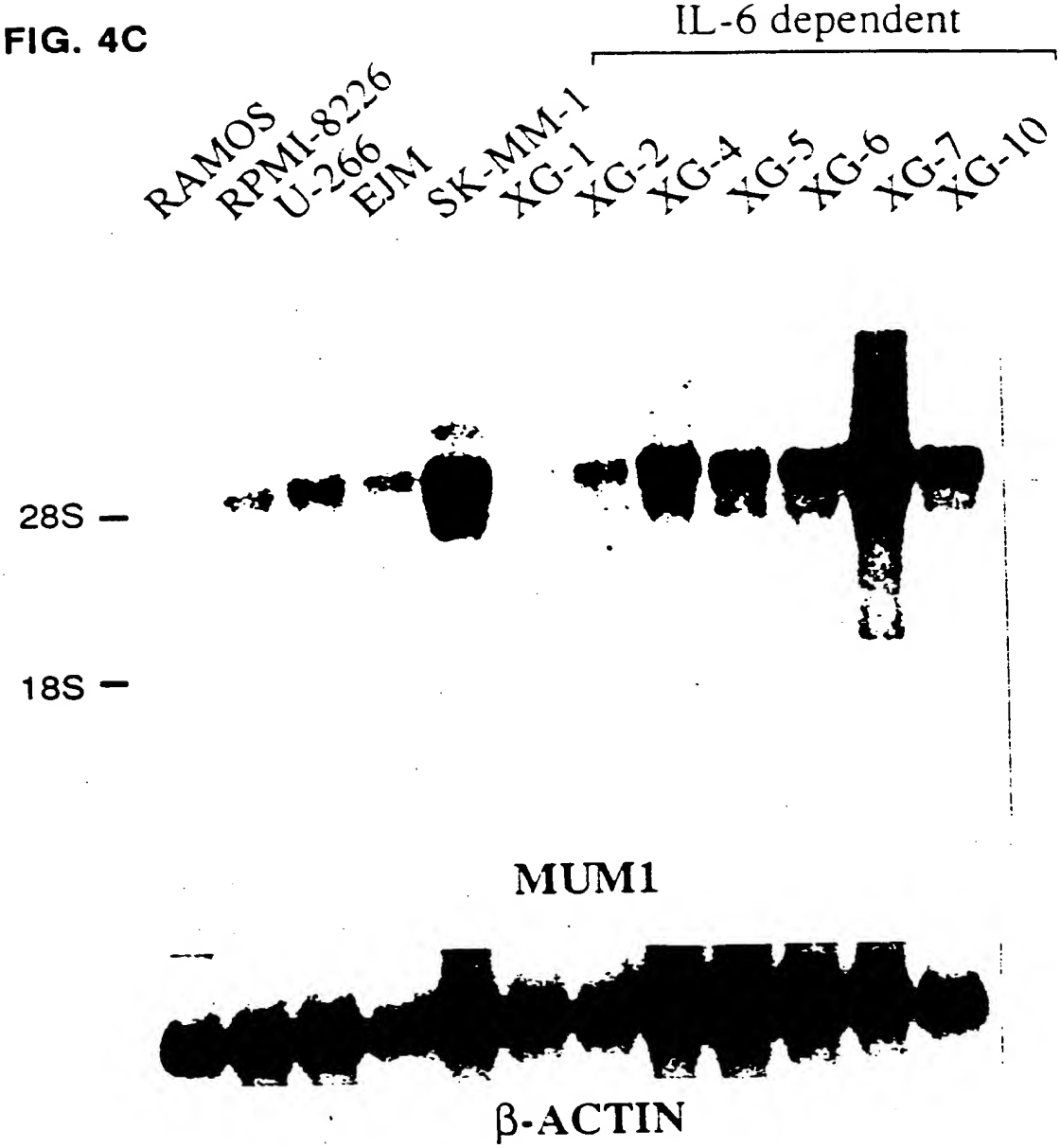

IL-6 dependent
RAMOS
RPMI-8226
U-266
EJM
SK-MM-1
XG-1
XG-2
XG-4
XG-5
XG-6
XG-7
XG-10
28S
18S
MUM1
β-ACTIN

FIG. 5A

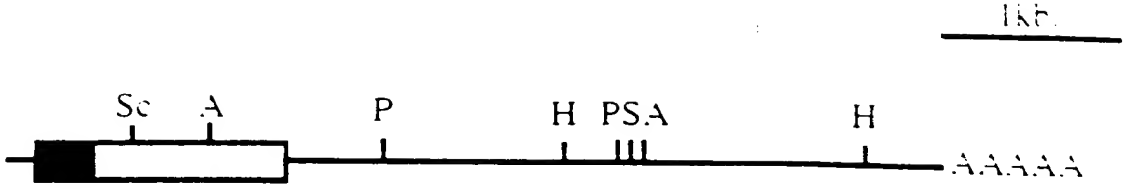


FIG. 5B-1

```
   1  GCCTGACCAA CATGGTAAAA CCCCATCTCT GCTAAAACTA CAAAAAAT
  51  GCTGGATGTG GTGGCAGGGA ACCTGTCATC CCAGCTAGTT GGGAGACT
 101  GGCAGGAGAA TCGCTCGATC TTGGGACCCA CCGCTGCCCT CAGCTCCG
 151  TCCAGGGCGA GTGCAGAGCA CAGCGGGCGG AGGACCCCGG GCGCGGGC
 201  GGACGGCACG CGGGGCATGA ACCTGGAGGG CGGCGGCCGA GGCGGAGA
                          M  N   L  E  G   G  G  R   G  G  E
 251  TCGGCATGAG CGCGGTGAGC TGCGGCAACG GGAAGCTCCG CCAGTGGC
        G  M  S   A  V  S   C  G  N  G   K  L  R   Q  W  L
 301  ATCGACCAGA TCGACAGCGG CAAGTACCCC GGGCTGGTGT GGGAGAAC
      I  D  Q  I   D  S  G   K  Y  P   G  L  V  W   E  N
 351  GGAGAAGAGC ATCTTCCGCA TCCCCTGGAA GCACGCGGGC AAGCAGGA
        E  K  S   I  F  R  I   P  W  K   H  A  G   K  Q  D
 401  ACAACCGCGA GGAGGACGCC GCGCTCTTCA AGGCTTGGGC ACTGTTTA
        N  R  E   E  D  A   A  L  F  K   A  W  A   L  F  K
 451  GGAAAGTTCC GAGAAGGCAT CGACAAGCCG GACCCTCCCA CCTGGAAG
      G  K  F  R   E  G  I   D  K  P   D  P  P  T   W  K
 501  GCGCCTGCGG TGCGCTTTGA ACAAGAGCAA TGACTTTGAG GAACTGGT
        R  L  R   C  A  L  N   K  S  N   D  F  E   E  L  V
 551  AGCGGAGCCA GCTGGACATC TCAGACCCGT ACAAAGTGTA CAGGATTG
        R  S  Q   L  D  I   S  D  P  Y   K  V  Y   R  I  V
 601  CCTGAGGGAG CCAAAAAAGG AGCCAAGCAG CTCACCCTGG AGGACCCG
      P  E  G  A   K  K  G   A  K  Q   L  T  L  E   D  P
 651  GATGTCCATG AGCCACCCCT ACACCATGAC AACGCCTTAC CCTTCGCT
        M  S  M   S  H  P  Y   T  M  T   T  P  Y   P  S  L
 701  CAGCCCAGCA GGTTCACAAC TACATGATGC CACCCCTCGA CCGAAGCT
        A  Q  Q   V  H  N   Y  M  M  P   P  L  D   R  S  W
 751  AGGGACTACG TCCCGGATCA GCCACACCCG GAAATCCCGT ACCAATGT
      R  D  Y  V   P  D  Q   P  H  P   E  I  P  Y   Q  C
 801  CATGACGTTT GGACCCCGCG GCCACCACTG GCAAGGCCCA GCTTGTGA
        M  T  F   G  P  R  G   H  H  W   Q  G  P   A  C  E
 851  ATGGTTGCCA GGTGACAGGA ACCTTTTATG CTTGTGCCCC ACCTGAGT
        G  C  Q   V  T  G   T  F  Y  A   C  A  P   P  E  S
 901  CAGGCTCCCG GAGTCCCCAC AGAGCCAAGC ATAAGGTCTG CCGAAGCC
      Q  A  P  G   V  P  T   E  P  S   I  R  S  A   E  A
 951  GGCGTTCTCA GACTGCCGGC TGCACATCTG CCTGTACTAC CGGGAAAT
        A  F  S   D  C  R  L   H  I  C   L  Y  Y   R  E  I
1001  TCGTGAAGGA GCTGACCACG TCCAGCCCCG AGGGCTGCCG GATCTCCC
        V  K  E   L  T  T   S  S  P  E   G  C  R   I  S  P
1051  GGACATACGT ATGACGCCAG CAACCTGGAC CAGGTCCTGT TCCCCTAC
      G  H  T  Y   D  A  S   N  L  D   Q  V  L  F   P  Y
1101  AGAGGACAAT GGCCACAGGA AAAACATTGA GAACCTGCTG AGCCACCT
        E  D  N   G  H  R  K   N  I  E   N  L  L   S  H  L
```

FIG. 5B-2

```
1151  AGAGGGGCGT GGTCCTCTGG ATGGCCCCCG ACGGGCTCTA TGCGAAAAC
        R  G  V    V  L  W    M  A  P  D    G  L  Y    A  K  R
1201  CTGTGCCAGA GCACGATCTA CTGGGACGGG CCCCTGGCGC TGTGCAACC
        L  C  Q  S    T  I  Y    W  D  G    P  L  A  L    C  N
1251  CCGGCCCAAC AAACTGGAGA GAGACCAGAC CTGCAAGCTC TTTGACACA
        R  P  N    K  L  E  R    D  Q  T    C  K  L    F  D  T
1301  AGCAGTTCTT GTCAGAGCTG CAAGCGTTTG CTCACCACGG CCGCTCCC
        Q  F  L    S  E  L    Q  A  F  A    H  H  G    R  S  L
1351  CCAAGATTCC AGGTGACTCT ATGCTTTGGA GAGGAGTTTC CAGACCCT
        P  R  F  Q    V  T  L    C  F  G    E  E  F  P    D  P
1401  GAGGCAAAGA AAGCTCATCA CAGCTCACGT AGAACCTCTG CTAGCCAG
        R  Q  R    K  L  I  T    A  H  V    E  P  L    L  A  R
1451  AACTATATTA TTTTGCTCAA CAAAACAGTG GACATTTCCT GAGGGGCT
        L  Y  Y    F  A  Q    Q  N  S  G    H  F  L    E  G  Y
1501  GATTTACCAG AACACATCAG CAATCCAGAA GATTACCACA GATCTATC
        D  L  P  E    H  I  S    N  P  E    D  Y  H  R    S  I
1551  CCATTCCTCT ATTCAAGAAT GAAAAATGTC AAGATGAGTG GTTTTCTT
        H  S  S    I  Q  E  *
1601  TCCTTTTTTT TTTTTTTTTT TTTGATACGG AGATACGGGG TCTTGCTC
1651  TCTCCCAGGC TGGAGTGCAG TGACACAATC TCAGCTCACT GTGACCTC
1701  CCTCCTGGGT TCAAGAGACT CTCCTGCCTC AGCCTCCCTG GTAGCTGG
1751  TTACAGGTGT GAGCCACTGC ACCCACCCAA GACAAGTGAT TTTCATTG
1801  AATATTTGAC TTTAGTGAAA GCGTCCAATT GACTGCCCTC TTACTGTT
1851  GAGGAACTCA GAAGTGGAGA TTTCAGTTCA GCGGTTGAGG AGAATTGC
1901  CGAGACAAGC ATGGAAAATC AGTGACATCT GATTGGCAGA TGAGCTTA
1951  TCAAAAGGAA GGGTGGCTTT GCATTTTCTT GTGTTCTGTA GACTGCCA
2001  ATTGATGATC ACTGTGAAAA TTGACCAAGT GATGTGTTTA CATTTACT
2051  AATGCGCTCT TTAATTTGTT GTAGATTAGG TCTTGCTGGA AGACAGAG
2101  AACTTGCCTT TCAGTATTGA CACTGACTAG AGTGATGACT GCTTGTAG
2151  ATGTCTGTGC CATTTCTCAG GGAAGTAAGA TGTAAATTGA AGAAGCCT
2201  CACGTAAAAG AAATGTATTA ATGTATGTAG GAGCTGCAGT TCTTGTGG
2251  GACACTTGCT GAGTGAAGGA AATGAATCTT TGACTGAAGC CGTGCCTG
2301  GCCTTGGGGA GGCCCATCCC CCACCTGCCA GCGGTTTCCT GGTGTGGG
2351  CCTCTGCCCC ACCCTCCTTC CCATTGGCTT TCTCTCCTTG GCCTTTCC
2401  GAAGCCAGTT AGTAAACTTC CTATTTTCTT GAGTCAAAAA ACATGAGC
2451  TACTCTTGGA TGGGACATTT TTGTCTGTCC TACAATCTAG TAATGTCT
2501  GTAATGGTTA AGTTTTCTTG TTTCTGCATC TTTTTGACCC TCATTCTT
2551  GAGATGCTAA AATTCTTCGC ATAAAGAAGA AGAAATTAAG GAACATAA
2601  CTTAATACTT GAACTGTTGC CCTTCTGTCC AAGTACTTAA CTATCTGT
2651  CCTTCCTCTG TGCCACGCTC CTCTGTTTGT TTGGCTGTCC AGCGATCA
2701  CATGGCGACA CTAAAGGAGG AGGAGCCGGG GACTCCCAGG CTGGAGAG
2751  CTGCCAGGAC CCACCACTGG AAGCAGGATG GAGCTGACTA CGGAACTG
2801  CACTCAGTGG GCTGTTTCTG CTTATTTCAT CTGTTCTATG CTTCCTCG
2851  CCAATTATAG TTTGACAGGG CCTTAAAATT ACTTGGCTTT TTCCAAAT
2901  TTCTATTTAT AGAAATCCCA AAGACCTCCA CTTGCTTAAG TATACCTA
2951  ACTTACATTT TTGTGGTTTT GAGAAAGTAC AGCAGTAGAC TGGGGCGT
```

FIG. 5B-3

```
3051  TCAGCAGAAG ATTGCGTTAG CTCTCAAATG TGTGTTCCTG CTTTTCTA
3101  GGATATTTTA AATTCATTCA ACAAGCACCT AGTAAGTGCC TGCTGTAT
3151  CTACATTACA CAGTTCAGCC TTTATCAAGC TTAGTGAGCA GTGAGCAC
3201  AAACATTATT TTTTAATGTT TAAAAAGTTT CTAATATTAA AGTCAGAA
3251  TTAATACAAT TAATATTAAT ATTAACTACA GAAAAGACAA ACAGTAGA
3301  ACAGCAAAAA AATAAAAAGG ATCTCCTTTT TTCCCAGCCC AAATTCTC
3351  CTCTAAAAGT GTCCACAAGA AGGGGTGTTT ATTCTTCCAA CACATTTC
3401  TTTTCTGTAA ATATACATAA ACTTAAAAAG AAAACCTCAT GGAGTCAT
3451  TGCACACACT TTTCATGCAG TGCTCTTTGT AGCTAAACAG TGAAGATT
3501  CCTCGTTCTG CTCAGAGGCC TTGCTGTGGA GCTCCACTGC CATGTACC
3551  GTAGGGTTTG ACATTTCATT AGCCATGCAA CATGGATATG TATTGGGC
3601  CAGACTGTGT TTCGTGAACT GCAGTGATGT ATACATCTTA TAGATGCA
3651  GTATTTTGGG GTATATTATC CTAAGGGAAG ATAAAGATGA TATTAAGA
3701  TGCTGTTTCA CGGGGCCCTT ACCTGTGACC CTCTTTGCTG AAGAATAT
3751  AACCCCACAC AGCACTTCAA AGAAGCTGTC TTGGAAGTCT GTCTCAGG
3801  CACCCTGTCT TCTTAATTCT CCAAGCGGAT GCTCCATTTC AATTGCTT
3851  TGACTTCTTC TTCTTTGTTT TTTTAAATAT TATGCTGCTT TAACAGTG
3901  GCTGAATTTT CTGGAAAATG CTTCTTGGCT GGGGCCACTA CCTCCTTT
3951  TATCTTTACA TCTATGTGTA TGTTGACTTT TTAAAATTCT GAGTGATC
4001  GGGTATGACC TAGGGAATGA ACTAGCTATG GAAATAACTC AGGGTTAG
4051  ATCCTAGCAC TTGTCTCAGG ACTCTGAAAA GGAACGGCTT CCTCATTC
4101  TGTCTTGATA AAGTGGAATT GGCAAACTAG AATTTAGTTT GTACTCAG
4151  GACAGTGCTG TTGAAGATTT GAGGACTTGT TAAAGAGCAC TGGGTCAT
4201  GGAAAAAATG TATGTGTCTC CCCAGGTGCA TTTTCTTGGT TTATGTCT
4251  TTCTTGAGAT TTTGTATATT TAGGAAAACC TCAAGCAGTA ATTAATAT
4301  CCTGGAACAC TATAGAGAAC CAAGTGACCG ACTCATTTAC AACTGAAA
4351  TAGGAAGCCC CTGAGTCCTG AGCGAAAACA GGAGAGTTAG TCGCCCTA
4401  GAAAACCCAG CTAGACTATT GGGTATGAAC TAAAAAGAGA CTGTGCCA
4451  GTGAGAAAAA TGTAAAATCC TACAGTGGAA TGAGCAGCCC TTACAGTG
4501  GTTACCACCA AGGGCAGGTA GGTATTAGTG TTTGAAAAAG CTGGTCTT
4551  AGCGAGGGCA TAAATACAGC TAGCCCCAGG GGTGGAACAA CTGTGGGA
4601  CTTGGGTACT CGCACCTCTT GGCTTTGTTG ATGCTCCGCC AGGAAGGC
4651  CTTGTGTGTG CGTGTCAGTT ACTTTTTTAG TAACAATTCA GATCCAGT
4701  AAACTTCCGT TCATTGCTCT CCAGTCACAT GCCCCCACTT CCCCACAG
4751  GAAAGTTTTT CTGAAGTGTT GGGATTGGTT AAGGTCTTTA TTTGTATTA
4801  GTATCTCCCC AAGTCCTCTG TGGCCAGCTG CATCTGTCTG AATGGTGC
4851  GAAGGCTCTC AGACCTTACA CACCATTTTG TAAGTTATGT TTTACATGC
4901  CCGTTTTTGA GACTGATCTC GATGCAGGTG GATCTCCTTG AGATCCTGA
4951  AGCCTGTTAC AGGAATGAAG TAAAGGTCAG TTTTTTTTGT ATTGATTTT
5001  ACAGCTTTGA GGAACATGCA TAAGAAATGT AGCTGAAGTA GAGGGGACG
5051  GAGAGAAGGG CCAGGCCGGC AGGCCAACCC TCCTCCAATG GAAATTCCC
5101  TGTTGCTTCA AACTGAGACA GATGGGACTT AACAGGCAAT GGGGTCCAC
5151  TCCCCCTCTT CAGCATCCCC CGTACC
```

FIG. 6A

```
MUM-1   (23-72)   KLRQWLIDQI DSGKYPGLVW ENEEKSIFRI PWKHAGKQDY NREEDAALFK
LSIRF   (23-72)   KLRQWLIDQI DSGKYPGLVW ENEEKSVFRI PWKHAGKQDY NREEDAALFK
IRF-1   (7-56)    RMRPWLEMQI NSNQIPGLIW INKEEMIFQI PWKHAAKHGW DINKDACLFR
IRF-2   (7-56)    RMRPWLEEQI NSNTIPGLKW LNKEKKIFQI PWMHAARHGW DVEKDAPLFR
ICSBP   (9-60)    RLRQWLIEQI DSSMYPGLIW ENEEKSMFRI PWKHAGKQDY NQEVDASIFK
ISGF3γ  (11-60)   KLRNWVVEQV ESGQFPGVCW DDTAKTMFRI PWKHAGKQDF REDQDAAFFK
IRF-3   (7-55)    RILPWLVSQL DLGQLEGVAW VNKSRTRFRI PWKHGLRQD. AQQEDFGIFQ

MUM-1   (73-122)  AWALFKGKFR EGIDKPDPPT WKTRLRCALN KSNDFEELVE RSQLDISDPY
LSIRF   (73-122)  AWALFKGKFR EGIDKPDPPT WKTRLRCALN KSNDFEELVE RSQLDISDPY
IRF-1   (57-106)  SWAIHTGRYK AGEKEPDPKT WKANFRCAMN SLPDIEEVKD QSRNKGSSAV
IRF-2   (57-106)  NWAIHTGKHQ PGVDKPDPKT WKANFRCAMN SLPDIEEVKD KSIKKGNNAF
ICSBP   (59-107)  AWAVFKGKFK EG.DKAEPAT WKTRLRCALN KSPDFEEVTD RSQLDISEPY
ISGF3γ  (61-109)  AWAIFKGKYK EG.DTGGPAV WKTRLRCALN KSSEFKEVPE RGRMDVAEPY
IRF-3   (56-104)  AWAEATGAYV PGRDKPDLPT WKRNFRSALN RKEGLRLAED RSK.DPHDPH

MUM-1   (123-130) KVYRIVPE
LSIRF   (123-130) KVYRIVPE
IRF-1   (107-114) RVYRMLPP
IRF-2   (107-114) RVYRMLPL
ICSBP   (108-115) KVYRIVPE
ISGF3γ  (110-117) KVYQLLPP
IRF-3   (105-112) KIYEFVNS
```

FIG. 6B

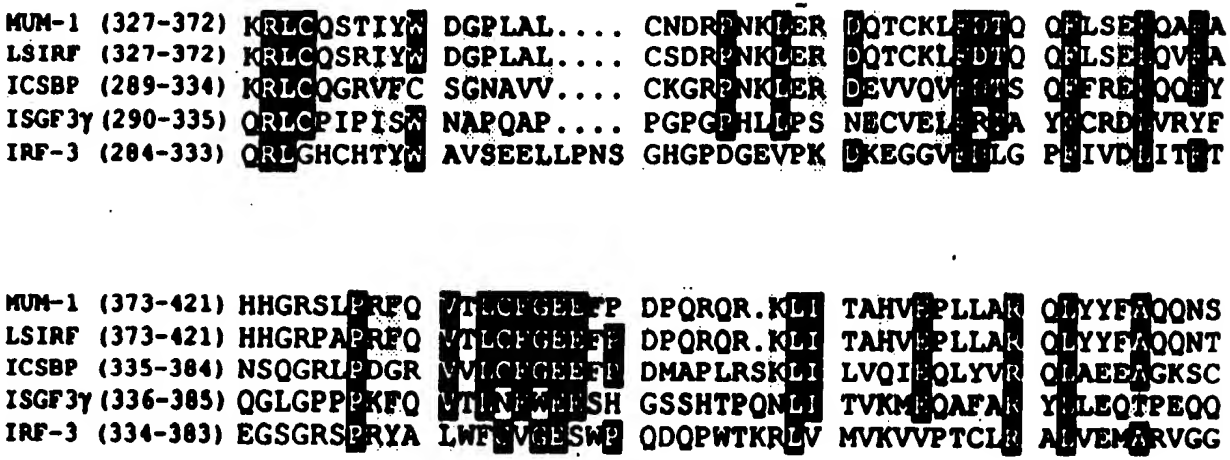
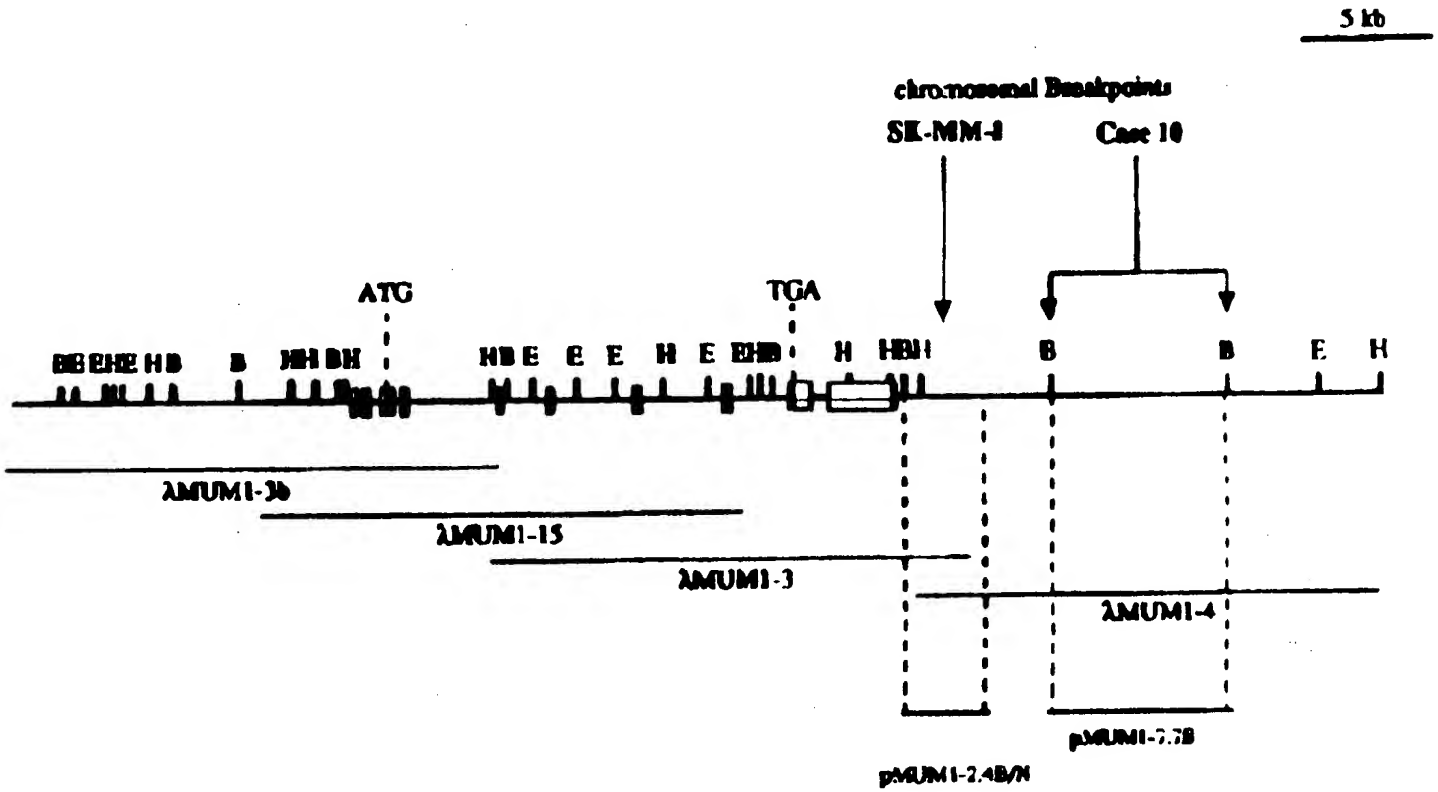

MUM-1 (327-372) KRLCQSTIYW DGPLAL.... CNDRPNKLER DQTCKLSDTQ QFLSEIQAIA
LSIRF (327-372) KRLCQSRIYW DGPLAL.... CSDRPNKLER DQTCKLSDTQ QFLSEIQVIA
ICSBP (289-334) KRLCQGRVFC SGNAVV.... CKGRPNKLER DEVVQVITTS QFFREIQQTY
ISGF3γ (290-335) QRLCPIPISW NAPQAP.... PGPGPHLLPS NECVELSRQA YFCRDIVRYF
IRF-3 (284-333) QRLGHCHTYW AVSEELLPNS GHGPDGEVPK DKEGGVSLLG PSIVDLITST
MUM-1 (373-421) HHGRSLPRFQ VTLCFGEEFP DPQRQR.KLI TAHVEPLLAR QLYYFAQQNS
LSIRF (373-421) HHGRPAPRFQ VTLCFGEEFP DPQRQR.KLI TAHVEPLLAR QLYYFAQQNT
ICSBP (335-384) NSQGRLPDGR VVLCFGEEFT DMAPLRSKLI LVQIEQLYVR QLAEEAGKSC
ISGF3γ (336-385) QGLGPPPKFQ VTLNFGEESH GSSHTPQNLI TVKMEQAFAR YLLEQTPEQQ
IRF-3 (334-383) EGSGRSPRYA LWFSVGESWP QDQPWTKRLV MVKVVPTCLR ALVEMARVGG

FIG. 7

Genomic locus spanning MUM1 gene



pMUM1- 7.7 B means the 7.7kb insert is BamHI sites .

B/N means BamHI/NotI site is used for cloning.
Every genomic inserts is cloned into pBluescript KS.

FIG. 8

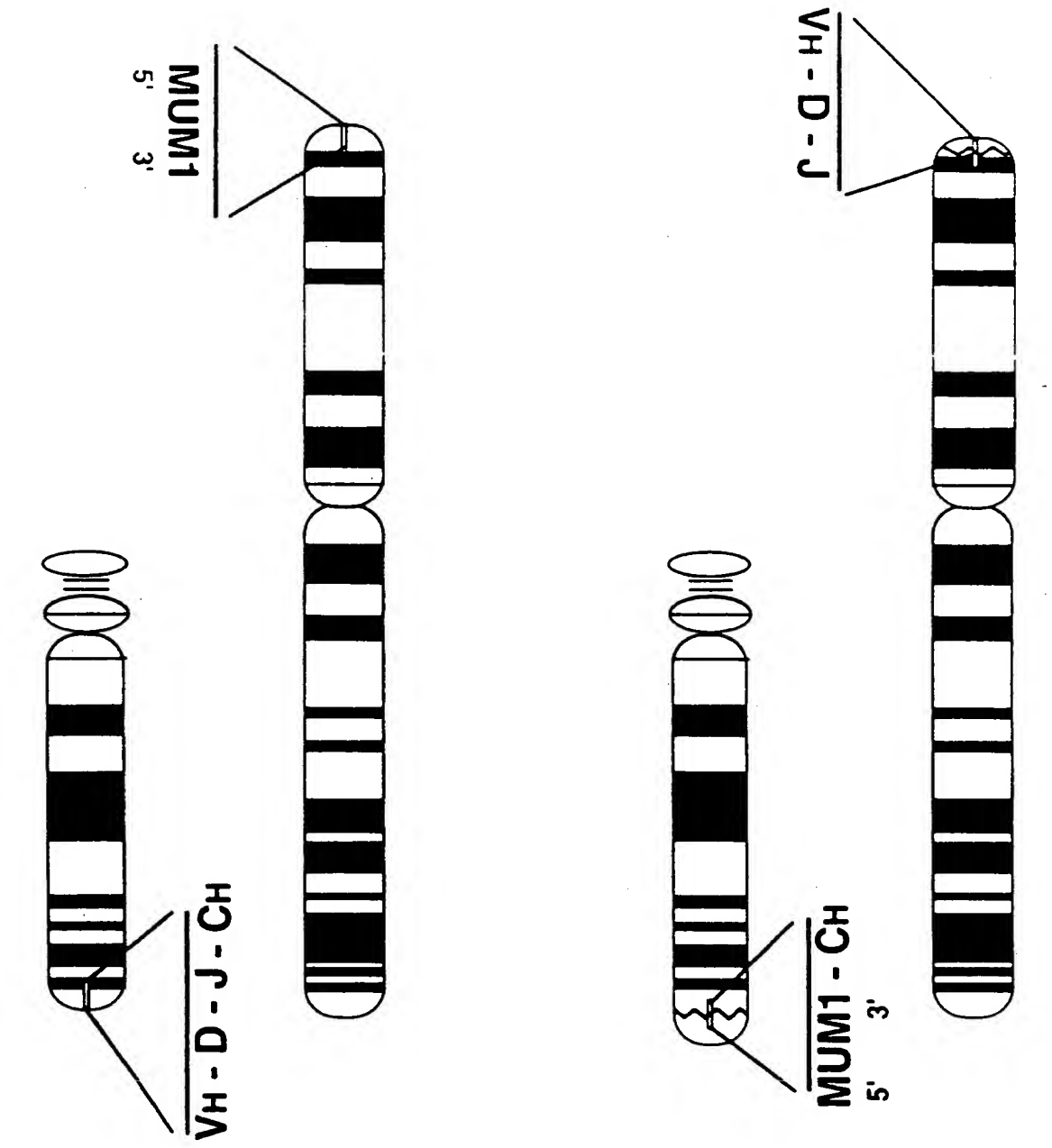


FIG. 9A

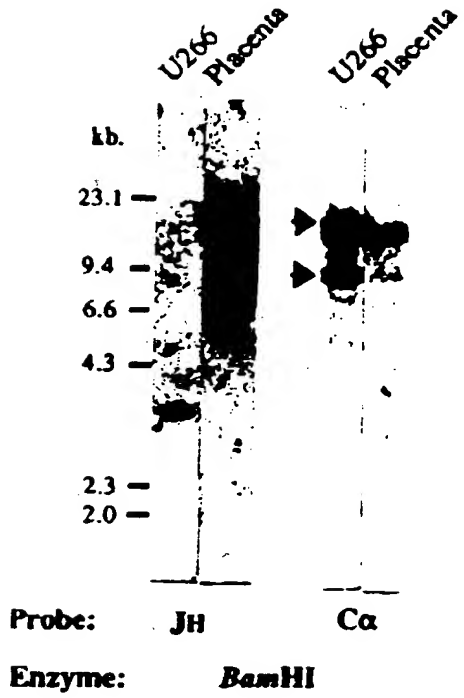
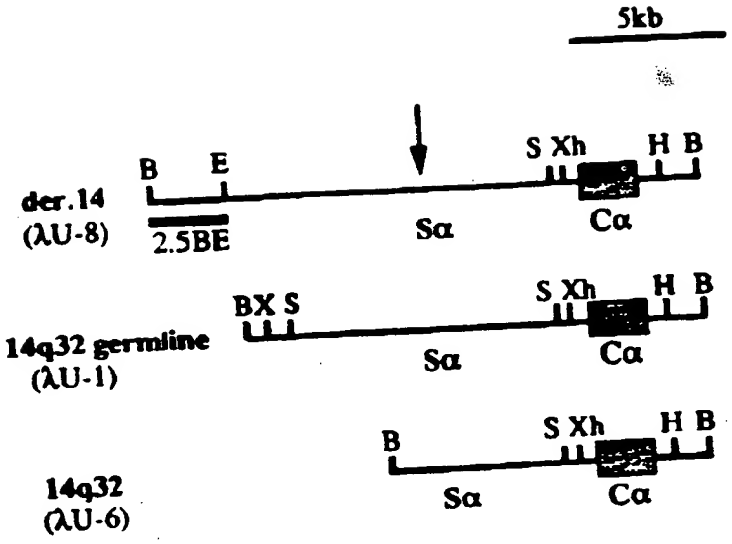

U266
Placenta
U266
Placenta
kb.
23.1
9.4
6.6
4.3
2.3
2.0
Probe:
JH
Cα
Enzyme:
BamHI

FIG. 9B



B, *Bam*HI; H, *Hin*dIII; S, *Sac*II; X, *Xba*I; Xh, *Xho*I

chromosomal breakpoint

FIG. 10

MUM2 **Transcripts detected in MM/PCL Cell Lines**

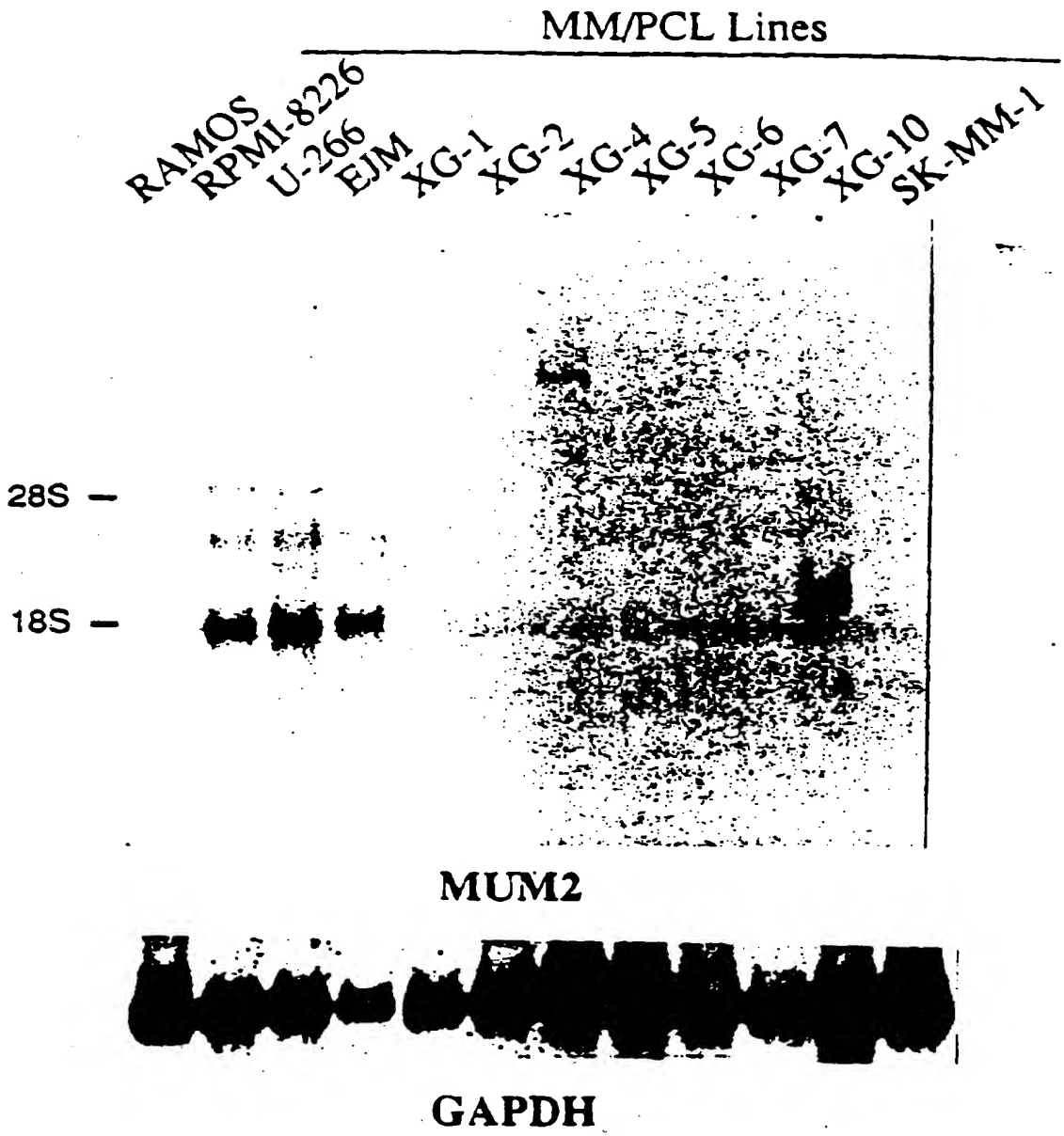


FIG. 11A

Physiological IgH gene rearrangement

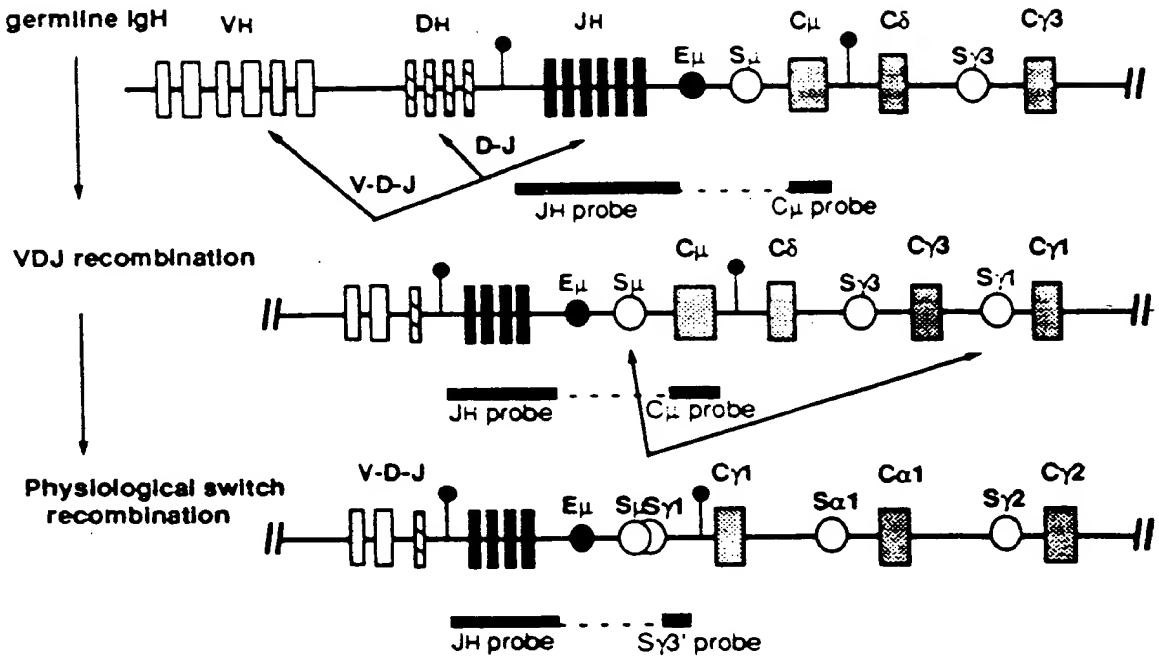
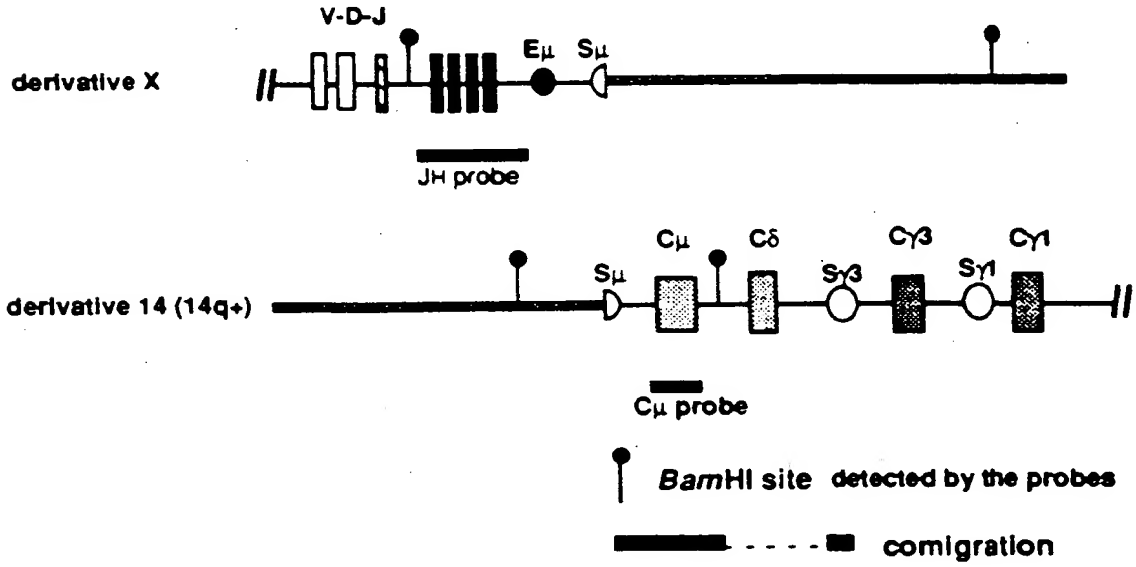
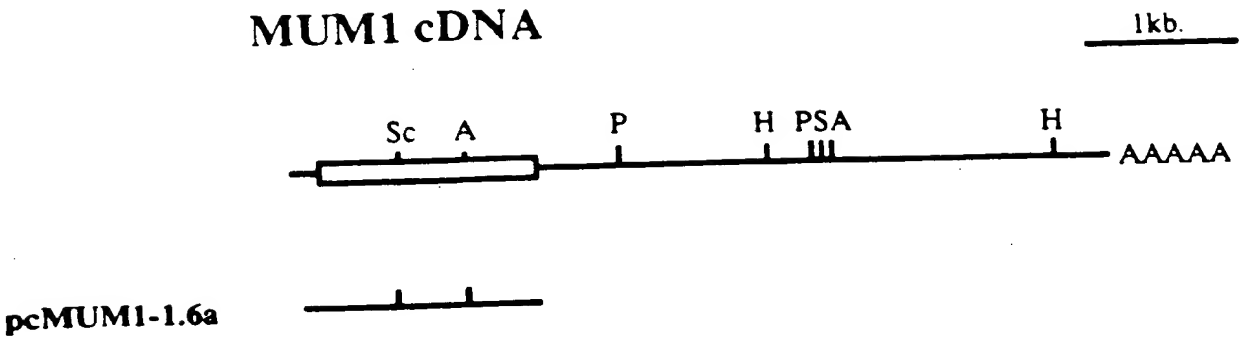


FIG. 11B

Chromosomal translocation occuring in switch region





Sc; SacII, P;*Pst*I, H;*Hin*dIII, S;*Sac*I, A;*Apa*I

cDNA inserts is cloned into EcoRI / BamHI site of the pBluescript KS+ Bacteria strain used is DH5α cells. pcMUM1-1.6a contains full length open reading frame of nt.217~1572.

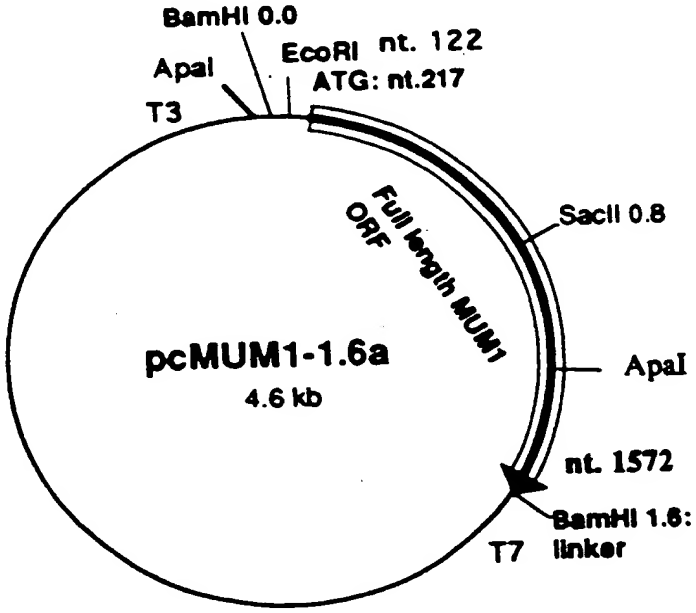
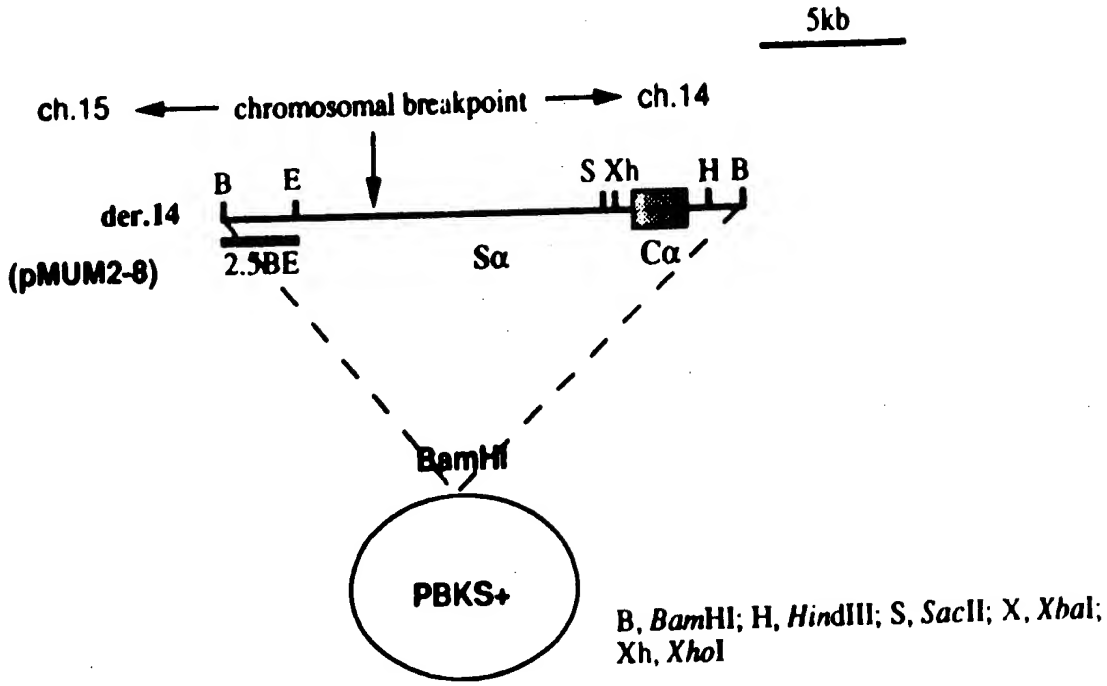


FIG. 12 A-B

Breakpoint Cloning of the U-266 Cell Line



pMUM2-8 has a 22.0kb insert in BamHI site of pBluescript KS+.

FIG. 13